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December 6, 2002, 23:33:11; Search time 1527.5 Seconds (without alignments) 16168.980 Million cell updates/sec
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1525
1 tctagaccatgtctggaaag......ccaactcagaagtagtcgac 1525
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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BST:*

: em_estba:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	**************************************	AF113676 HOMO SAPI	AKOOSEST Wis miscur	DEDIN SUM COSCOUNT	BOKA3710 ACENOCIDE	BO64890 AGENCORIE
SUMMARIES	DI	AF130068			AK004999	BO643710	BQ648909
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æ			28.3	21.7	20.9	20.3	20.0
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BQ653587 BM924019 BQ646142 BQ958958 BM924813 BQ650189 BQ646948 BQ646948	BQ007663 BQ064738 BQ650502 AV649258 BQ644130 BG554467	BO064473 BO064473 BO06453778 BO0645533 BIZ19058 BIZ50698 BG50698 BG50698 BG566873 AII14643 AII14643 AII28000 BIZ59000 BIZ59000 BIZ59000 BIZ59000	BQ182052 AII10706 BI246204 BG218001 BM724546 BM724546 AIS26727 BI761275 BQ646994
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988886777			16.2 16.1 16.0 16.0 16.0 16.0 16.0 16.0 16.0
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ALIGNMENTS

AF130068 2478 bp mRNA linear HTC 08-MAY-2001 AF130068 1 GI:11493442 HTC. HTC. HTC. HTC. HTC. HTC. HTC. HTC.	Mammalla: Eutherla: Primates, Crairates, Verebiates; Eutergoscomis, Mammalla: Eutherla: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2478) Zhang,C., Yu.Y., Zhang,S., Wel,H., Bi.J., Zhou,G., Dong,C., Zai,Y., Xu,W., Gao,F., Liu,M., and He,F. Functional prediction of the coding sequences of 75 new genes deduced by analysis of CDNA clones from human fetal liver	oupulished 2 (bases 1 to 2478) 2 hang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y., Xu, W., Gao, F., Liu, M. and He, F. Direct Submission Submitted (23-FEB-1999) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China	
RESULT 1 AF130068 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUFCE

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Homo sapiens.
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PTENKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDETLLE
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VFSNGADLSGYTEEAPLKLSRAVKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNN
PFVFLMIEQNTKSPLEMGKVVNPTQK"
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                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 2478;
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                                         1082. .2338
/note="predicted protein of HQ2209"
                                                                                                                                                                                                                                                                                                                                                                                            Score 433.2; DB 11;
Pred. No. 4.9e-101;
0; Mismatches 493;
                                                                                                /evidence=not_experimental/product="PRO2209"
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/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                        597 g
                                                                                   /codon_start=1
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Best Local Similarity 59.7%;
Matches 729; Conservative (
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2571)
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CTACTGCTATTTTTTTTTTACCAGACGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137
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                                                                                                                                                                                                                                                                                                                                                                                   AF113676 2571 bp mRNA linear HTV
Homo saplens clone FLB2803 PROD684 mRNA, complete cds.
AF113676
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PRVFLAMGRONTSPLENGKVVNNFTQK*

638 C 556 G 577 t
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59.6%; Pred. No. 1.3e-100;
/evidence=not_experimental
/product="PRO0684"
/protein_id="AAF29581.1"
/db_xref="G1:6855601"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus adult male kidney cDNa, RIKEN full-length enriched library, clone:0610011G14:serine protease inhibitor 1-4, full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                               CTCATGACATTATTACTAAATTTTTAGAGAACGAGGATCGTCGTAGCGCTTCTCTGCACC
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High efficiency full-length cDNA cloning
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'dev_stage="adult"
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                       Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Gisuco, T., Saito, T., Saito, T., Saito, T., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Magner, L., Washio, T., Sakai, K., Okido, T., Fuzuki, R., Tomita, M., Waner, L., Washio, T., Sakai, K., Okido, T., Fuzuki, R., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Stoobach, C., Seya, T., Shibata, Y., Stocch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Wilming, L., Wanshizaki, Y., Shibata, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Kawaji, H., Kohtsuki, S. Nanga, A., Mature, M., Mature, G., Wang, K., Kawaji, H., Kohtsuki, S. Angara, A., Mature, M., Mature, C., Wallin, M., Mature, G., Mature, C., Wallin, M., Mature, G., Wang, K., Mature, G., Wang, K., Wang, M., Wang, K., Wang, K
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Adachi, J., Aizawa, K., Bono, H., Brownstein, M., Bult, C.,
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
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Hume, D., Imotani, K., Ishli, Y., Itoh, M., Koya, K.,
Kato, H., Kawai, J., Kojima, Y., Konno, H., Koya, M., Koya, S.,
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D.,
Sogabe, Y., Sakai, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I.,
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Submitted (10-JUJ-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="FANTOM_DB:0610011G14"
/db_xref="MGD:MGI:1896776"
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ATULGOFALRLYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNL
TQTSEADIHKSFQHLLQTLNRPDSELOLSTGNGLFVNNDLKHVBFRLERAKNHYQAEV
FSVRPAESEBKKYINDFVEKGTGGKIVEAVKKLDODTVFALANYILFKGKWKOPFDP
FSVRTEAEFFHVDESTTVKVPPMTLSGMLDVHHCSMLSKWLLMDYAGNTTAVFLLPDDG
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DLSGITEENAPLKKLSKAVHKAVLTIDETGTEAAAATVLQVATYSMPPIVRFDHPFLFI
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/translation="MTPSISWSLLLLAGLCCLVPSFLAEDVOETDTSQKDQSPASHEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GCTCTCCCTAGGGAGCAAGGGTGACACTCACACGCAGATCCTAGAGGGCCTGCAGTTCAA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 TCAAAGTAATTCTACTAACATTTTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCAT 523
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/note="data source:MGD, source key:MGI:891968,
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                                                                     1064 GTATTTAGGTAACGCTACTGCTATTTTTTTTTACCAGGAAGGTAAGGTTCAACATTT 1123
                                                                                                                                                                           1124 AGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGATCGTCGTAG 1183
                                                                                                                                                                                                                                                                            1184 CGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTT 1243
                                                                                                                                                                                                                                                                                                                            970 IGCICAGAICCAIAICCCCAGACIGICCAICICIGGAAACIAIAACIIGAAGACACICAI 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                1030 GACTCCACTGGGCATCACCGGATCTTCAACAATGGGGCTGACCTCTCCGGAATCACAGA 1089
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                                                                                                                                                                                                                         AK004999 1296 bp mRNA linear HTC 19-JAN-
Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300014A17:serine protease inhibitor 1-4, full
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Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
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Hah-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
AK004999.1 GI:12836611
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** Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishil, Y., Arakawa, T., Hara, A., Fukunshi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I. Salto, T., Osjobori, T., Bondo, S., Yamanaka, I. Salto, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kuchi, P., Lewis, S., Yamano, M., Cissi, C., Kina, B., Kochiwa, H., Kuchi, P., Lewis, S., Yamano, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrimi, L.M., Staubil, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarili, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Hane, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Kingwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. Punctional annotation of a full-length mouse cDNA collection NE 200556
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RS Adachi, J. Alzawa K., Akahira, S., Akimura, T., Aono, H., Aral, A., Arakwa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukudishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Imctani, K., Ishli, Y., Itah, M., Izawa, M., Kasukwa, T., Hume, D., Imctani, K., Ishli, Y., Konno, H., Koya, S., Koya, S., Konno, H., Koya, S., Koya, S., Konno, H., Koya, S., Koya, S., Konno, H., Koya, S., Konno, H., Koya, S., Sakai, C., Sakai, 
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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AUTHORS
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/translation="MTPSISWCLLLAGLCCLVPSFLAEDVQETDTSQKDQSPASHEI
ATNLGDPAISLYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILBGLQFNL
ATNLGDPAISLYRELVHQSNTSNIFFSPVSIATAFAMLSLGSKGDTHTQILBGLQFNL
PCYDEADIHNGFOHLLQTINRPDSELGQLSTGWGHEVNBNDLKLVBFKLEBAKHHYQAEV
FSVNFABSEEAKKVINDFVEKGTQGKIVEAYKKLEQDTYFVLANTILFKGRWKKPFDP
BNTKQABEHVDSSTTYKYPMMTLSGMLDVHHCSTLSSWVLLMDYAGNATAVFLLPDDG
KMQHLEQTINKELISKFLLNRRRRLAQIHIPPLSISGNYNLETLMSPAGA
DLSGITEENAPLKLSQAVKAVUTIDETGTEAAAATVLQGGFLSMPPILHFNRPFLFI
IFEEHSGSPLFVVDPTHK"

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                          /tissue_type="liver"
/done_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 CCATGAGATTGCTACAAACCTGGGAGACTTTGCCATCAGTCTATACCGGGAGCTGGTCCA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 TCAAAGTAATTCTACTAACATTTTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 TCAAGGCGACGCCGCTCAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 TCTGGCTGAGGATGTTCAGGAGACAGACACCTCCCAGAAGGATCAGTCC---CCAGCCTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 GTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGTTTTAGAAGGTTTAAAACTTTAA
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                                                                                                                                                                                                                        /gene="Spil-4"
/note="data source:MGD, source key:MGI:891968,
evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vred. NO. 1.7e-71;
0; Mismatches 517; Indels
                                                                                                                                                                                                                                                                                                                                 serine protease inhibitor 1-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="MGD:MGI:891968"
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/clone="1300014A17"
                                                                                                                                                                /gene="Spil-4"
                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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Best Local Similarity 55.6%;
Matches 655; Conservative
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BO643710 887 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8342217 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6268225
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1304 AG----AAGCTCCATTAAAAITGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATTGATGA 1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1244 AGGCCAGTTAGGTATTACCAAAGTTTTTTTTTTAACGGTGCCGATTTGAGTGGTGTTACTGA 1303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1361 AAAGGGTACCGAGGCGCCGGCGCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACC 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1130 GACAGGAACAGAAGCIGCAGCAGCIACAGICTTACAAGGCGGTITITIGICTAIGCCCCC 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1124 AGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGATCGTCGTAG 1183
                                                                                                     1004 ACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTATTAATGAA 1063
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
770 CTCGGGCATGCTTGACGTGCACCATTGCAGCACGCTCCCAGCTGGGTGCTGCTGATGGA
                                                                                                                                                                                                                                                                                                                    1184 CGCITCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTT
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Contact: Robert Strausberg, Ph.D.
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/tissue_type="hepatocellular carcinoma, cell line"
/hab_host="hH10B (phage-resistant)"
/hote="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAGGGG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
it.m."
IRT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                                                                                                                                                                           519 GCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAAAC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        579 ITTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTGAGA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTITGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTGTCT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     759 GCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTT 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GCCTTCACTGTCAACTTCGGGACACCGAAGAGGCCCAAGAACAGATCAACGATTACGTG 300
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Best Local Similarity 60.0%; Pred. No. 3.1e-69;
Matches 532; Conservative 0; Mismatches 354; Indels 1; Gaps
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/clone_lib="NIH_MGC_l00"
/tissue_type="hepatocellular carcinoma, cell line"
/tasue_type="hepatocellular carcinoma, cell line"
/tas.bost="DH108 (phage-resistant)"
/note="Organ: liver; vector: porB7; Site_1: xho!; Site_2:
EcoR1, cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/XhoI sites using the following 5' adaptor:
GGCAGGG(G): Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Garald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                            907 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8351269 NIH_MGC_100 Homo sapiens cDNA clone LMAGE:6286839
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stranford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2488 row: e column: 16
High quality: sequence stop: 721.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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2 others
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/db_xref="taxon:9606"
/clone="IMAGE:6286839"
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AGENCOURT_8349591 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:6284550
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NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                             TCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATATT
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Contact: Robert Strausberg, Ph.D.
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="bH10B (phage-resistant)" site_1: XhoI; Site_2:
/note="Organ: liver: Vector: pOTB7; Site_1: XhoI; Site_2:
into EcoRI.XhoI ande by oligo-dr priming Directionally cloned
into EcoRIXhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500pp for average insert size
GGCACGAG(G). Size-selected by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
in RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 5.3e-64;
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                                       /clone="IMAGE:6284550"
/clone_lib="NIH_MGC_100"
/organism="Homo sapiens"
                   /db_xref="taxon:9606"
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Best Local Similarity 59.3%;
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/note="Organ: Document of the color, kidney, stomach; vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size range 1.3 kb. Library is normalized and entiched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                           BM924019
985 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6709923 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760183
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NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammallan Gene Collection (MGC) Contact: Robert Strausberg, Ph.D.
777 ACATCCAGCACTGTAAGAAGCTGTCCAGCTGGTGCTGATGAAATACCTGGGGCATG 836
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
http://mage.llnl.gov
http://mage.llnl.gov
Plate: LLAM12806 row: m column: 16
High quality sequence stop: 707.
Location/Qualifiers
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                                                                               tch 18.8%; Score 287; DB 14; Length 985; al Similarity 59.5%; Pred. No. 2.6e-63; 519; Conservative 0; Mismatches 351; Indels
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Tissue Procurement: Life Technologies, Inc.
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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BQ646142
AGENCORT_8492569 NIH_MGC_100 Homo saplens cDNA clone IMAGE:6296341
BQ646142
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                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CONA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2504 row: a column: 14
234 CCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGA 293
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                                              CTAAAGCCGATACCCATGACGAGTTTTAGAAGGTTTAAACTTTAATTTGACCGAAATCC
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                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
High quality sequence stop: 647.
Location/Qualifiers
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/do_xrel="taxon:j900"
/clone='InMacc_40"
/clone='InMacc_40"
/tissue_type="carcinoma"
/tissue_type="carcinoma"
/tissue_type="carcinoma"
/lab_host="bull0B (phage=resistant)"
/note="organ: prostate; vector: poTB7; Site_1: XhoI;
/note="organ: prostate; vector: poTB7; Site_1: XhoI;
/note="organ: prostate; vector: poTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
/stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

1 others
                                                                                                                                                                                                                                                                                                     924 bp mRNA linear EST 21-AUG-2002 AGENCOURT_10034701 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6483305 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
62 receaseageaceaararerrerrereceasigageareseracaseerrrecaarsere 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequenting by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGc clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gow.k column: 18 plate: LLCM2667 row: k column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 924)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                              1406 AATGAGCATTCCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGA 1455
                                                                                                                                                                  0; Mismatches 363; Indels
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 586.
Location/Qualifiers
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AGENCOURT_6653921 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761267 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        1128 AATGAGTTGACTCATGACATTATTACTAAATT--TTTAGAGAACGAGGATCGTCGTAGCG 1185
                                                                                                                                                                                                                                                                       948 GAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAGACTG 1007
                                                                                                                                                                                                                                                                                                                        1008 GGTATGTTCAATATTCAACATTGCAAAAATTAAGTTCTTGGGTCTTATTAATGAAGTAT 1067
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182 ACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAAC 241
                        648 CAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTTGTCTGAAGGTTTA 707
                                      708 AAATIGGIIGACAAAITCCIAGAAGACGICAAGAAACIAIAICAIAGIGAGGCITIIACC 767
                                                                                      GTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGC 827
                                                                                                                                       828 ACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTA 887
                                                                                                                                                                                      GTTAACTATATTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAA 947
                                                                                                                                                                                                                                     602 GCCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTGCTGATGAAATAC 661
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia! Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1194)
                                                                                                                                                                                                                            Email: cgapbs-rémail.nin.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Homo sapiens
                                                                                                                                                                         JOURNAL
COMMENT
                                                                                                                  AUTHORS
                                                                                   REFERENCE
                                                                                                                                               TITLE
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/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MC Library."
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                                                                                                    /clone="IMAGE:5761267"
/clone_lib="NIH_MGC_116"
                                                              /organism="Homo sapiens"
High quality sequence stop: 662.
                                                                                    /db_xref="taxon:9606"
                        Location/Qualifiers
                                                                                                                                               /lab_host="DH10B"
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/clone="IMAGE:6269613"
/clone_lhb="IMAGE:6269613"
/clone_lhb="MiR_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
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                                                                                                                                                                                                9U/ bp mRNA linear EST 15-JUL-2002
S', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabar Temail.nih.gov
EMA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://mage.lih.gov
Plate: LLCM2443 row: g column: 22
High quality sequence stop: 650.
Location/Coualifiers
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NIH-MGC http://mgc.nci.nlh.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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JOURNAL
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                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
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BQ646948
AGENCOURT_8302495 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:6271313
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stranford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2447
Tow: n. column: 18
High quality Sequence Stop: 672.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1260 ACCAAAGTITITTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAAAA 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1140 CATGACATTATTACTAAATTTTTAGAGAACGAGGATCGTCGTAGCGCTTCTGTGCACCTG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1200 CCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTAGGCCAGTTAGGTATT 1259
                                                                                                                                                                                                              960 CATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAAGACTGGGTATGTTCAAT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                        1020 ATICAACAITGCAAAAATTAAGTICITGGGTCTIATTAATGAAGTATTTAGGTAACGCT 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1080 ACTGCTATTTTTTTTTTACCAGACGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGACT 1139
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National Institutes of Health, Mammalian Gene Collection (MGC)
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900 TITITCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGGAAGATTTT 959
                                                                                                       247 TICTITAAAGGCAAATGGGAGAGACCCTITGAAGTCAAGGACACCGAGGAAGAGGACTIC 306
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/db_xref="taxon:9606"
/clone="IMAGE:6271313"
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="bH10B (phage-resistant)"
/note="lorgan: liver; Vector: pOPFB; Site_1: XhoI: Site_2:
ECCRI; cDNA made by oligo-dT priming. Directionally: cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAGGG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of Callifornia, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
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                                                                                                                                                                                                                                                                                                                                                                                            298 TGTGTGGTAAGTCCTGTGTTTCCCCAGTCAAGGCCATGGAAGACCCTCAAGGCGACGCCG 357
                                                                                                                                                                                                                                                                                                                                                                                                                        358 CTCAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTTTAATAAAATTACTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 CCAACCIGGCIGAGTICGCCTICAGCCIATACCGCCAGCIGGCACACCAGTCCAGCAGACAGCA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              898 ITITITCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGA-AGAGGAAGAT 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 TCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGGAAGAGGAC 709
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                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 59.4%; Pred. No. 2.7e-59;
Matches 495; Conservative 0; Mismatches 336; Indels 2;
                                                                                                                                                                                                                                                      189 t
clone_lib="NIH_MGC_100"
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6269919"
/clone_lib="NHH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="BulloB (phage-resistant)"
/note="Organ: liver; vector: pOTB7; Site_1: xhoI; Site_2:
FCORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI; About sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8%b. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California. Berkeley)
using ZaP-cDNA synthesis kit (Stratagene) and Superscript
ribrary."
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                959 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8297828 NIH_MGC_100 Homo saplens cDNA clone IMAGE:6269919 5', mRNA sequence.
BQ648524 BG648524.1 GI:21772696
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 959)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
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829 GGCAACGCCATCTTCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAA 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 270.4; DB 14; Length 959; 59.3%; Pred. No. 5.1e-59; tive 0; Mismatches 326; Indels 1;
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High quality sequence stop: 674.
Location/Qualiflers
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AUTHORS
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us-10-025-514-7.rst

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BG567260 796 bp mRNA linear EST 10-APR-2001 602589741F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723498 5',
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/clone="IMAGE:472498"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1170 GAGGATCGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGA- 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1229 CITAAAATCIGIITTAGGCCAGITAGGIAITACCAAAGIITITITITAAAAGGGGGCGGAITI 1288
                                                                                                                                                                                                                                                                                                                       1110 AAGCTICAACATITAGAGAAIGAGTIGACICAIGACAITATIACTAAAITTITAGAGAAC 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              рe
                                                                                                                                                                                                                                        990 CCAATGATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 GAAGACAGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGAT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                         GAGGTTAAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTT 989
                                                                                                                                                                                                421 GAAGTCAAGGACACCGAGGAAGAGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTG 480
                                                                                                                                                                                                                                                               361 GACACAGITITIGCICIGGIGAATIACAICITITIAAAGGCAAAIGGGAGAGACCIIT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnh.gov
Plate: LLCMI583 row: b column: 11
High quality sequence stop: 730.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
810 GATTATGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGT
                                                                              870 GATACCGTCTTCGCACTAGTTAACTATATTTTTTAAGGGTAAGTGGGAACGTCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .796
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1289 GAGTGGTGTTACTGAAGAAGCTCC 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 CCCCGGGGGTCACAGAGGAACGCC 804
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BG567260
BG567260.1 GI:13574913
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Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATANGCCC-3' and 3' adaptor sequence: 5'-CACGGCCGACATG-dT(30)BN-3' (where B = A, 5', Or G and N = A, C, G, Or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1099 CAGACGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAAT 1158
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                                                                                                                                                                                                                                                                                                                                                                                                 61 TCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAATATCTTCTTCTTCTCCCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    499 TITCIAITGCCACTGCITITCGCCATGTTGAGITTAGGTACTAAAGCCGATACCCATGACG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 ATCACGACCAAGACCATCCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTT 438
                                                                                                                                                                                                                                                                                                                                                               439 ITTCTITGTATAGACAATTAGCTCATCAAGTAATTCTACTAACATTTTTTTAGTCCTG 498
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859 AATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATTTTTTTCAAGGGTAAGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTTCAAGAGTTGTTGAGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTG
                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                      Length 796;
                                                                                                                                                                                                                                                         0; Mismatches 317; Indels
                                                                                                                                                                                                                        17.6%; Score 268; DB 12; 60.0%; Pred. No. 2e-58;
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